

Research Article

Gene Expression in Leaves and Epidermis of Arabidopsis under Salt and Drought Stress

Khalifa S. Mohamed^{1*}, Ahlam Rashed², A.M. EL-Mahmoudy², Adel M Abdallaa Shrefe², Nouri Kushlaf², Seham¹ and T.M. Oshkondali³

¹University of Al-Jabal Elgharbi Libya

²Faculty of Science /Zawia University, Libya

³Faculty of Medicine / Zawia University, Libya

*Corresponding Author

Khalifa S. Mohamed

Abstract: Gene expression induced by drought and salt stress. Also, difference genes in different time are induced with different stresses. Plants of Arabidopsis were divided into groups one under salt stress and others are to drought for 6h. Most genes are expression in both leaves and epidermis under both treatments. However, DREB2A was more highly expression in leaves at control and epidermis at 2h of drought stress as compared with other treatments.

Keywords: Plants of Arabidopsis, DREB2A.

INTRODUCTION

Sever environmental stress can be responsible for up to 65% reduction in plant yield, salt and drought stresses are two of the major factors which cause this (Serrano 1999). Drought and salt stresses can be connected because drought can cause soil to become salty directly or indirectly through irrigation. Growth rates are lower and biomass accumulates more slowly in roots under salt stress For example, when barley was exposed to 100 mM NaCl and 0.1mM Ca⁺ growth and development were reduced, including reduced root hair density and root thickening compared with control plants (Shabala *et al.*, 2003). The most obvious factors to explain the reduction in plant growth is exposure to salt where the osmotic stress and Na⁺ toxicity affect the mineral nutrition (Reid and Smith 2000). Expression some genes has been shown to increase in response to salinity, cold, drought and oxidative stress (Fang *et al.*, 2015).

Gene expression is often different between organs and between stresses. For example *DREB2A* and *DREB2B* genes are highly expressed in roots in response to high salt and dehydration while in stems only in response to dehydration. *DREB2A* and *DREB2B* genes have weak expression in leaves of Arabidopsis while *RD29a* was highly expressed in

roots, stems and leaves after 5 hours dehydration. Also the expression of *DREB2A* and *DREB2B* were weak in flowers and siliques, and the expression of *COR78/RD29a* was also observed (Nakashima *et al.*, 2000).

MATERIALS AND METHODS

Plants of *Arabidopsis thaliana* L.(Heyn) ecotype Columbia were grown in the control condition for about 5 to 6 weeks of sowing. The temperature used was 20°C /15°C for day/night. Samples were collected for analysis at the same time when plants were transferred to other treatments (time 0). The samples were collected in 1.5 ml micro centrifuge tubes, frozen in liquid nitrogen, and stored at -80°C until needed.

For salt treatment, compartments containing plants growing in soil were immersed in solution containing 250 mM NaCl for 15-20 minutes. For drought treatment, the leaves were collected in Petri dishes and the leaves were weighed immediately after cutting from the plants.

Epidermis or peeled leaves were used. Lower epidermis was peeled off using tweezers. samples of peeled epidermis or whole leaf were collected and put in micro tubes. About 15-25 mg was collected from

Quick Response Code



Journal homepage:

<http://www.easpublisher.com/easjals/>

Article History

Received: 25.10.2019

Accepted: 06.11.2019

Published: 15.11.2019

Copyright © 2019 The Author(s): This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International License (CC BY-NC 4.0) which permits unrestricted use, distribution, and reproduction in any medium for non-commercial use provided the original author and source are credited.

DOI: 10.36349/easjals.2019.v02i11.002

epidermis and 100-150mg from leaves and used to analyze different periods of exposure to salt and drought stress. RNA extracted using TRI reagent and gene expression analysis by PCR

RESULTS AND DISCUSSION

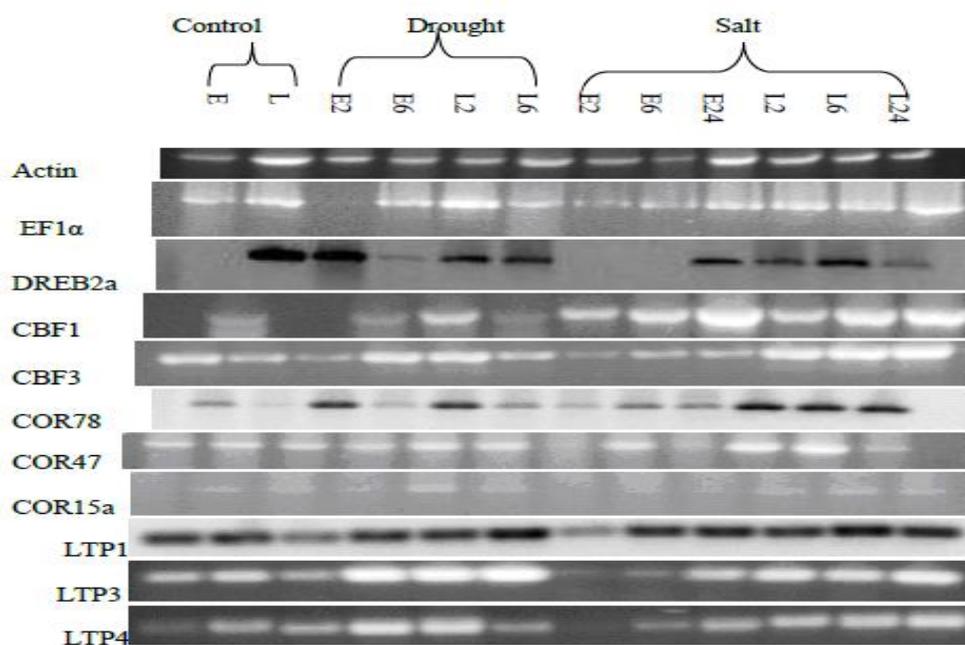
The results have shown that gene expression for constitutively expressed reference genes *Actin* and *EF1α* and also for transcription factor *COR* and *LTP* genes at 2 h and 6 h during drought and at 2 h, 6 h and 24 h under salt stress. The *actin* gene was expressed in both leaves and epidermis. The expression was lower in the epidermis at control, epidermis 2 h salt and epidermis 6 h salt. However, *EF1α* was expressed in most samples but it was undetectable in epidermis at 2 h drought and also it was weak in epidermis at 2 h of salt.

DREB2a was expressed in control leaves and sample leaves at 2 h and 6 h of drought and 2 h, 6h and 24 h under salt stress (Fig 1). It was highly expressed in epidermis at 2 h under drought, it was more than in leaves under drought. It was undetectable at 2 h and 6 h salt in epidermis. On the other hand it was detectable at 24 h in epidermis under salt. *CBF1* was expressed under drought stress in epidermis at 6 h and in leaves at 2 h

compared with control levels. *CBF1* had a higher expression in epidermis at 24 h in salt and in leaves at 24 h in salt compared with the control. *CBF3* was detectable in all samples. It showed higher expression, in the epidermis at 6 h and in leaves at 2 h, than other samples in drought stress. It had a higher expression in leaves than epidermis under salt stress.

COR78 was expressed when plants were exposed to drought in both leaves and epidermis at 2 h but expression decreased at 6 h in both leaves and epidermis (Fig 1). However, the expression was higher in leaves than epidermis under salt stress.

Most researchers have analysed acclimation in whole plants and organs but gene expression induced by cold is different in plant tissues, for example epidermis and vascular transition zone in cereals (Pearce *et al.*, 1998). In plants, about 60 to 77% of the genes do not have a strict tissue expression (Okamura and Goldberg, 1989). many genes are co-ordinately regulated by salt and drought stress, supporting a high degree of cross talk between these types of stresses (Rabbani *et al.*, 2003; Nakashima *et al.*, 2009).



Fig(1)PCR products using cDNA from 100ng total RNA extracted from epidermis and leaves from Arabidopsis exposed to 2 h and 6 h drought or exposed to salt for 2 h, 6 h and 24 h. E= epidermis, L= leaves.

REFERENCES

1. Fang, Y., Liao, K., Du, H., Xu, Y., Song, & H., Li, X. (2015). A stress-responsive NAC transcription factor SNAC3 confers heat and drought tolerance through modulation of reactive oxygen species in rice. *J. Exp. Bot.* 66, 6803–6817.
2. Nakashima, K., Ito, Y., & Yamaguchi-Shinozaki, K. (2009). Transcriptional reg-ulatory networks in response to abiotic stresses in Arabidopsis andgrasses. *Plant Physiol*149:88–95.
3. Nakashima, K., Shinwari, Z.K., Sakuma, Y., Seki, M., Miura, S., Shinozaki, K., & Yamaguchi-Shinozaki, K. (2000). Organization and expression of two Arabidopsis DREB2 genes encoding DRE-binding proteins involved in dehydration- and high-salinity-responsive gene expression. *Plant Molecular Biology* 42: 657-665.

4. Rabbani, M.A., Maruyama, K., Abe, H., Khan, M.A., Katsura, K., Ito, Y., Yoshiwara, K., Seki, M., Shinozaki, K., & Yamaguchi-Shinozaki, K. (2003). Monitoring expression profiles of rice genes under cold, drought, and high-salinity stresses and abscisic acid application using cDNA micro-array and RNA gel-blot analyses. *Plant Physiology* 133:1755–1767.
5. Reid, R.J., & Smith, F.A. (2000). The limits of sodium/calcium interactions in plant growth. *Australian Journal of Plant Physiology* 27: 709-715.
6. Serrano, R., Culianz-Macia, F.A., Moreno, V. (1999). Genetic engineering of salt and drought tolerance with yeast regulatory genes. *Scientia Horticulturae* 78: 261-269.
7. Shabala, S., Shabala, L., Van-Volkenburgh, E. (2003). Effect of calcium on root development and root ion fluxes in salinised barley seedlings. *Functional Plant Biology* 30: 507-514.